

## SEQ.ST25 SEQUENCE LISTING

<110> Gonzalgo, Mark L.

Jones, Peter A.

Liang, Gangning

<120> CANCER DIAGNOSTIC METHOD BASED UPON DNA METHYLATION DIFFERENCES

<130> 47675-21

<140> 09/887,941

<141> 2001-06-22

<150> US 09/094,207

<151> 1998-06-09

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 530

<212> DNA

<213> homo sapiens

<400> 1

cccgcgacct aagccagcga cttaccacgt tagtcagcta agaagtggca gagctgggat 60 tcgaacctat aaagaactct gaagcctggg tattttaca tgacacttta cataatgcgc 120 cacggggtag tcggagggg aggtccatct ccctttccct tgctgtccat ctccacagaa 180 aagaagcaag tggaggacag gagccagaaa gtcatctggc cgcggatcat tccggagtga 240

ccccgccgc	caccactcgc	atagtccgct	SEQ.ST tatggcggga		gagattctca	300
caggggctgt	gcggccagaa	ccagaagtgc	aaagcaccgt	tagcgactct	atcgccccct	360
gccgcctgtg	gcgcccagtc	cgaagctgct	gttttcagga	gggctagtgg	gctaagaaaa	420
gagctcaccg	actgactgcc	caacagctgt	tgcgagccag	tgctaggctg	cagacagcct	480
tgccaaatgt	ggtgacataa	gcgggagggg	ggaacattta	gagagcccta		530
<210> 2						
<211> 308						
<212> DNA						
<213> homo	o sapiens					
<400> 2 ctagggtagg	ctggtctgtg	ctggatacgc	gtgttcttct	gcggagttaa	agggtcgggg	60
acgggggttc	tggacttacc	agagcaattc	cagccggtgg	gcgtttgaca	gccacttaag	120
gaggtaggga	aagcgagctt	caccgggcgg	gctacgatga	gtagcatgac	gggcagcagc	180
agcagcagcc	agcaaaagcc	tagcaaagtg	tccagctgct	gcactgccgc	ggggactccc	240
acatcaccat	gactagttgt	gcaactctgc	agcagaaacg	gcttccgagg	aacacaggat	300
cgcggggg						308
<210> 3						
<211> 177						
<212> DNA						
<213> homo	o sapiens					
<400> 3 gcttcctttt	tctcggcttt	cctcactatc	ctctccctgt	tcgagagtat	ctccaccagc	60
accgagcctc	acacgggctg	tgcctccatc	tttggaatgc	ctacccttct	ttcttgcgaa	120
gcccctccca	gggccagccc	ttgtgcaccg	gctcaagggg	actgctctcc	tgcctcg	177
<b>2010</b>						
<210> 4						
<211> 148						

<212> DNA

## <213> homo sapiens $\cdot$

<400> 4						
ttgcgccgat	cgtcaagaac	ctctcatccc	tggcagcagc	aaagccaata	tatttccatt	60
tcttatttca	gtttgccacc	aaaacaaagc	tgcgcgcggc	tgagggcagg	aaggcgctga	120
gaccgaccga	gaagaaggga	cgtcccgg				148
<210> 5						
<211> 384			•			
<212> DNA						
<213> hom	o sapiens					
<400> 5 caggcccgcc	gagactccac	tccaactacc	aggaaatttc	ccgtggagct	tcaattcctg	60
ggaccctcct	actgcgggga	gagtggtttc	cctgccccac	accatgccct	aggcccgagt	120
ctgcggctct	tgggggatct	ctccgagctc	cgacaccgtg	ttcggaccgg	gtgcgccctg	180
ccgctggggc	tcaagcctgc	aggcgtgaga	accgggggac	tctctatggc	accaagagct	240
tcaccgtgag	cgtaggcaga	agcttcgctt	tgatcctagg	gcttacaaag	tcctcctttg	300
gctgcccatg	atggtaaaag	ggcagttgct	cacaaagcgc	gagtgtgtgt	gccagacagt	360
gtaaatgagt	gttgggaccg	gcgt				384
<210> 6						
<211> 178						
<212> DNA	,					
<213> hom	o sapiens					
<400> 6 gggtccgttc	gtgaatgcat	gagcagggtg	tgagcgccag	ggggttacac	ttctcacggg	60
ttaaaaccca	gacaacttca	cgagggaacc	acgtgccatt	ttaacagcgt	acggtcggga	120
tcgtgggacg	tcattaaacg	gagtgggttg	agtatgtgac	tctgtcaccc	attttctg	178
<210> 7						
<211> 359	ı					

## SEQ.ST25

<212> DNA

<213> homo sapiens	
<400> 7	
ccccgcgggg cagaatccaa gtgagtcaga cacattgctc cctccctgct gctgccagtc	60
catctctttg ccaacaaacc tgcttaaaat gccaaagctg gtccaaagtt tcaggaaaac	120
aacttccgcc agagggcacg tagagggcac agatgctata gatgcttctc tgacaaacac	180
tectgacece ettgacagat tggaaaatae atggtteaga aagggtgaga gattteaact	240
tgagaagtga aactaggaaa agatggaagg tgtccggatt tctagctcaa gtccacacac	300
tgcttctgct gcggtgacta aatcgtggct gtgttctcat cacctgcctc gcggcgcgc	359
<210> 8	
<211> 251	
<212> DNA	
<213> homo sapiens	
<400> 8	<i>C</i> (
ggcgggcctg ggcaccgcgg aggggggct tttctgcgcc cggcgaagcg tggaacttgc	60
	120
cgccccagtg cagatgctgt gagcttagac gaggacaggg catggcactc ggcttggccc	180
gtagtggacg gtgtttttgc agtcatgaac ccaaacgccg caaaccttga ccgtttcccc	240
acccgtgttg t	251
<210> 9	
<211> 145	
<212> DNA	
<213> homo sapiens	
<220>	
<221> misc_feature	
<222> (126)(126)	

## SEQ.ST25 <223> a, g, c or t sequence variation may exist at this position <220> <221> misc feature <222> (127)..(127) <223> a, g, c or t sequence variation may exist at this position <400> 9 tgagagcagc atcctccct gcgtgtggtt ctctaactta cctcctgtat ggggtctgcg 60 gacccagcac acctcccggg cccccaaaaa attccagctc aagagcccta aaaatcctta 120 145 ccctgnnaaa gtttgagctt ctccc <210> 10 <211> 215 <212> DNA <213> homo sapiens <400> 10 acgccggcca cagttettea gtgaaacget teactetetg gteatagagg taggaaacta 60 tagctgtccc aactaaatgt caggacgaat tagcccagct ggtcacgctc acagtcaccg 120 cctccaccag actgagcgac cctcccaacg gggtttgccg tgttgggagg acagcggagt 180 ttcgttgctg tgtcaatttg tgtagacgcg gctgc 215 <210> 11

<400> 11
ctgctctctt ctcttcttt cccctttcct ctcctctcc tttcctcagg tcacagcgga 60
gtgaatcagc tcggtggtgt ctttgtcaac gggcggccac tgccggactc cacccggcag 120
aagattgtag agctagctca cagcggggcc cggccgtgcg acatttcccg aattctgcag 180

<211> 220

<212> DNA

<213> homo sapiens

	SEQ.ST25				
gtgatcc	tcc cggcgccgcc ccactcgccg cccccgcggc .	220			
<210>	12				
<211>	196				
<212>	DNA				
<213>	homo sapiens				
	12 acg gagggagtca ggagtgagcc cgaagatgga gagaagtcga ttcgcccaga	60			
	aga cggtggatca gagatgagtc ccaggaacct cagagagcga ggctgacagg	120			
	aga ggaccgggca gggacaaacc agcggacaga gcagagcgcg aaatggttga	180			
	aag cgacct	196			
<210>	13				
<211>	22				
<212>	DNA				
<213>	Artificial Sequence				
<220>					
<223>	p16 promoter region-specific Ms-SNuPE primer				
	13				
gtaggtg	ggg aggagtttag tt	22			
<210>	14				
<211>	23				
<212>	DNA				
<213>	Artificial Sequence				
<220>					
<223>	p16 promoter region-specific Ms-SNuPE primer				
	14	0.0			
エクセココセコ	acc aaccaaccc tcc	23			

<210>	15 .	
<211>	21	
<212>	AND	
<213>	Artificial Sequence	
<220>		
<223>	p16 promoter region-specific Ms-SNuPE primer	
<400>	15 tgtt tggaaagata t	21
	tyce tygaaayata t	21
<210>	16	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	p16 promoter region-specific Ms-SNuPE primer	
<400>	16 gggt gttatatt	18
cccag	ggge geedede	1.0
<210>	17	
<211>	15	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	p16 promoter region-specific Ms-SNuPE primer	
<400>	17 ggat agggt	1 =